

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:SSSPTAU188MXM

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * Welcome to STN International * * * * *

NEWS 1 Web Page URLs for STN Seminar Schedule - N. America
NEWS 2 "Ask CAS" for self-help around the clock
NEWS 3 SEP 01 INPADOC: New family current-awareness alert (SDI) available
NEWS 4 SEP 01 New pricing for the Save Answers for SciFinder Wizard within
STN Express with Discover!
NEWS 5 SEP 01 New display format, HITSTR, available in WPIDS/WPINDEX/WPIX
NEWS 6 SEP 27 STANDARDS will no longer be available on STN
NEWS 7 SEP 27 SWETSCAN will no longer be available on STN
NEWS 8 OCT 28 KOREAPAT now available on STN
NEWS 9 NOV 18 Current-awareness alerts, saved answer sets, and current
search transcripts to be affected by CERAB, COMPUAB, ELCOM,
and SOLIDSTATE reloads

NEWS EXPRESS OCTOBER 29 CURRENT WINDOWS VERSION IS V7.01A, CURRENT
MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
AND CURRENT DISCOVER FILE IS DATED 11 AUGUST 2004

NEWS HOURS STN Operating Hours Plus Help Desk Availability
NEWS INTER General Internet Information
NEWS LOGIN Welcome Banner and News Items
NEWS PHONE Direct Dial and Telecommunication Network Access to STN
NEWS WWW CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that
specific topic.

All use of STN is subject to the provisions of the STN Customer
agreement. Please note that this agreement limits use to scientific
research. Use for software development or design or implementation
of commercial gateways or other similar uses is prohibited and may
result in loss of user privileges and other penalties.

* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 16:39:40 ON 23 NOV 2004

=> file ca, biosis. medline

'BIOSIS.' IS NOT A VALID FILE NAME

Enter "HELP FILE NAMES" at an arrow prompt (=>) for a list of files
that are available. If you have requested multiple files, you can
specify a corrected file name or you can enter "IGNORE" to continue
accessing the remaining file names entered.

ENTER A FILE NAME OR (IGNORE):.

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
0.21	0.21

FULL ESTIMATED COST

FILE 'CA' ENTERED AT 16:39:57 ON 23 NOV 2004

USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.

PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2004 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'MEDLINE' ENTERED AT 16:39:57 ON 23 NOV 2004

=> file ca, medline, biosis
COST IN U.S. DOLLARS

	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.80	1.01

FILE 'CA' ENTERED AT 16:40:05 ON 23 NOV 2004
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2004 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'MEDLINE' ENTERED AT 16:40:05 ON 23 NOV 2004

FILE 'BIOSIS' ENTERED AT 16:40:05 ON 23 NOV 2004
Copyright (c) 2004 The Thomson Corporation.

=> s archaeal polymerase
L1 4 ARCHAEOAL POLYMERASE

=> d 1-4 ab, bib

L1 ANSWER 1 OF 4 CA COPYRIGHT 2004 ACS on STN
AB RNA polymerase from the hyperthermophile archaeon *Pyrococcus furiosus* (Pfu) forms specific and transcriptionally active complexes with its conjugate transcription factors TBP (the archaeal TATA binding protein homolog) and TFB (the archaeal homolog of eukaryotic RNA polymerase II and III transcription factors TFIIB and Brf) at the Pfu glutamate dehydrogenase promoter. A photochem. crosslinking method was used to map vicinity of the catalytic subunits of Pfu RNA polymerase to DNA locations distributed along the polymerase-promoter interface. The largest component of this **archaeal polymerase** is split into two subunits, A' and A'', whose relatively sharp boundary of DNA crosslinking (probed on the transcribed strand) is centered five to six base pairs downstream of the transcriptional start site. A strong argument based on this information, on the well-defined homol. between the core bacterial, archaeal and eukaryotic RNA polymerase subunits, and on the recently determined structure of a bacterial RNA polymerase specifies the directionality of DNA in the archaeal transcription complex and its trajectory downstream of the transcriptional start site.

AN 134:142663 CA
TI The orientation of DNA in an archaeal transcription initiation complex
AU Bartlett, Michael S.; Thomm, Michael; Geiduschek, E. Peter
CS Department of Biology and Center for Molecular Genetics, University of California, La Jolla, CA, 92093-0634, USA
SO Nature Structural Biology (2000), 7(9), 782-785
CODEN: NSBIEW; ISSN: 1072-8368
PB Nature America Inc.
DT Journal
LA English

RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L1 ANSWER 2 OF 4 MEDLINE on STN
AB RNA polymerase from the hyperthermophile archaeon *Pyrococcus furiosus* (Pfu) forms specific and transcriptionally active complexes with its conjugate transcription factors TBP (the archaeal TATA binding protein homolog) and TFB (the archaeal homolog of eukaryotic RNA polymerase II and III transcription factors TFIIB and Brf) at the Pfu glutamate dehydrogenase promoter. A photochemical crosslinking method was used to map the vicinity of the catalytic subunits of Pfu RNA polymerase to DNA

locations distributed along the polymerase-promoter interface. The largest component of this **archaeal polymerase** is split into two subunits, A' and A", whose relatively sharp boundary of DNA crosslinking (probed on the transcribed strand) is centered five to six base pairs downstream of the transcriptional start site. A strong argument based on this information, on the well-defined homology between the core bacterial, archaeal and eukaryotic RNA polymerase subunits, and on the recently determined structure of a bacterial RNA polymerase specifies the directionality of DNA in the archaeal transcription complex and its trajectory downstream of the transcriptional start site.

AN 2000455673 MEDLINE

DN PubMed ID: 10966650

TI The orientation of DNA in an archaeal transcription initiation complex.

CM Comment in: Nat Struct Biol. 2000 Sep;7(9):703-5. PubMed ID: 10966630

AU Bartlett M S; Thomm M; Geiduschek E P

CS Department of Biology and Center for Molecular Genetics, University of California, San Diego, La Jolla, California 92093-0634, USA..
bartlett@biomail.ucsd.edu

SO Nature structural biology, (2000 Sep) 7 (9) 782-5.

Journal code: 9421566. ISSN: 1072-8368.

CY United States

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals; Space Life Sciences

EM 200009

ED Entered STN: 20001005

Last Updated on STN: 20001005

Entered Medline: 20000928

L1 ANSWER 3 OF 4 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN

AB Deamination of cytosine to uracil in a G-C base pair is a major promutagenic event, generating G-C to A-T mutations if not repaired before DNA replication. Archaeal family B DNA polymerases are uniquely able to recognize unrepaired uracil in a template strand and stall polymerization upstream of the lesion, thereby preventing the irreversible fixation of an A-T mutation. We have now identified a 'pocket' in the N-terminal domains of archaeal DNA polymerases that is positioned to interact with the template strand and provide this ability. The structure of this pocket provides interacting groups that discriminate uracil from the four normal DNA bases (including thymine). These groups are conserved in **archaeal polymerase** but absent from homologous viral polymerases that are unable to recognize uracil. Using site-directed mutagenesis, we have confirmed the biological role of this pocket and have engineered specific mutations in the Pfu polymerase that confer the ability to read through template-strand uracils and carry out PCR with dUTP in place of dTTP.

AN 2003:81516 BIOSIS

DN PREV200300081516

TI Structural basis for uracil recognition by archaeal family B DNA polymerases.

AU Fogg, Mark J.; Pearl, Laurence H.; Connolly, Bernard A. [Reprint Author]

CS School of Cell and Molecular Biosciences, University of Newcastle, Newcastle upon Tyne, NE2 4HH, UK
b.a.connolly@ncl.ac.uk

SO Nature Structural Biology, (December 2002) Vol. 9, No. 12, pp. 922-927. print.

ISSN: 1072-8368 (ISSN print).

DT Article

LA English

ED Entered STN: 6 Feb 2003

Last Updated on STN: 6 Feb 2003

L1 ANSWER 4 OF 4 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN

AB RNA polymerase from the hyperthermophile archaeon *Pyrococcus furiosus*

(Pfu) forms specific and transcriptionally active complexes with its conjugate transcription factors TBP (the archaeal TATA binding protein homolog) and TFB (the archaeal homolog of eukaryotic RNA polymerase II and III transcription factors TFIIB and Brf) at the Pfu glutamate dehydrogenase promoter. A photochemical crosslinking method was used to map the vicinity of the catalytic subunits of Pfu RNA polymerase to DNA locations distributed along the polymerase-promoter interface. The largest component of this **archaeal polymerase** is split into two subunits, A' and A", whose relatively sharp boundary of DNA crosslinking (probed on the transcribed strand) is centered five to six base pairs downstream of the transcriptional start site. A strong argument based on this information, on the well-defined homology between the core bacterial, archaeal and eukaryotic RNA polymerase subunits, and on the recently determined structure of a bacterial RNA polymerase specifies the directionality of DNA in the archaeal transcription complex and its trajectory downstream of the transcriptional start site.

AN 2000:490391 BIOSIS

DN PREV200000490512

TI The orientation of DNA in an archaeal transcription initiation complex.

AU Bartlett, Michael S. [Reprint author]; Thomm, Michael; Geiduschek, E. Peter

CS Department of Biology and Center for Molecular Genetics, University of California, San Diego, La Jolla, CA, 92093-0634, USA

SO Nature Structural Biology, (September, 2000) Vol. 7, No. 9, pp. 782-785. print.

ISSN: 1072-8368.

DT Article

LA English

ED Entered STN: 15 Nov 2000

Last Updated on STN: 10 Jan 2002